SEQUENCE LISTING

SEQ ID No 1. - HCV Core Protein

/ SEQ IS IN II THEY CONCINCTION																				
GGTGCTTGCGAGTGCCCCGGGAGGTCTCGTAGACCGTGCACCATGAGCACGAATCCTAAA CCACGAACGCTCACGGGGCCCTCCAGAGCATCTGGCACGTGGTAGTCGTGCTTAGGATTT											360									
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			٠											M	S	Т	N	Р	K	6
CCTCAAAGAAAACCAAACGTAACACCAACCGTCGCCCACAGGACGTTAAGTTCCCGGGT										420										
GGAGTTTCTTTTTGGTTTGCATTGTGGTTGGCAGCGGGTGTCCTGCAATTCAAGGGCCCA																				
	_																	P	G	26
P	Q	R	K	Т	K	R	N	Т	N	R	R	P /	/Q	D	V	K	F	Р	G	20
GGCGGTCAGATCGTTGGTGGAGTTTACTTGTTGCCGCCCAGGGGCCCTAGATTGGGTGTG											480									
CCGCCAGTCTAGCAACCACCTCAAATGAACAACGGCCCGTCCCCGGGATCTAACCCACAC																				
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CGCGCGACGAGGAGACTTCCGAGCGGTCGCAACCTCGAGGTAGACGTCAGCCTATCCCC												540								
GCGCGCTGCTCCTTCTGAAGGCTCGCCAGCGTTGGAGCTCCATCTGCAGTCGGATAGGGG																				
		Т	R	K	T	s	E	R	S		P	R	G	R	R	0	P	I	P	66
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AAG									,											600
TTC	CGT	GCA	GCC	GGG'	TTC	CCG'	TCC'	TTG.	ac/co	CGA	GTC	GGG	CCC	ATA	GGA	ACC	GGG	GAG	ATA	
	А		R	P	K	G	R	N		A					P		P	L	Y	86
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											660									
GCAATGAGGGTTGCGGGTGGCCGGCTTGCCCCCAGTGGCTCTCGGCCTAGT CCGTTACTCCCAACGCCCACCCGCCCTACCGAGGACAGGGGGTCACCGAGAGCCGGATCA											660									
C ⊈ G'	TTA	CTC	CCA	ACG	CCC.	ACC	CGC	C¢T.	ACC	GAG	GAC.	AGG	GGG	TCA	.CCG	AGA	GCC	GGA'	ГСА	
ß	N	E	G	С	G	M	A	/G	W	L	L	S	P	S	G	S	R	P	S	106
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ACC	CCG	GGG'	TTG	CTG	GGG	GCT	GCA'	TCC.	AGC	GCG	TTA	AAC	CCA	TTC	CAG	TAG	CTA	1.GG	GAA	
W	G	P	N	D	P	R	/R	R	S	R	N	L	G	K	V	Ι	D	\mathbf{T}	L	126
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ACG	тсс	GGC'	ттс	GTC	CAT	CT/C	ΔТС	ദദദ	тъс	מידמ	CCG	СТС	GTC	GGC	GCC	CCT	CTT.	AGA	GGC	780
																	GAA			
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Т	C	G	F	V	D/	/ L	M	G	Y	Ι	P	L	V	G	A	Ρ	L	R	G	146
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GCTGCCAGGGCCCTGGGGCATGGCGTCCGGGTTCTGGAAGACGGTGTGAACTATGCAACA										840										
CGACGGTCCCGGGACGCCTACCGCAGGCCCAAGACCTTCTGCCACACTTGATACGTTGT																				
Α	Α	R	Α	L	/ _A	Н	G	V	R	V	L	E	D	G	V	N	Y	Α	T	166
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GGTAACCTTCCTGGTTGCTCTTTCTCTATCTTCCTTCTGGCCCTGCTCTCTTGCCTGACT											900									
CCATTGGAAGGACCAACGAGAAAGAGATAGAAGGAAGACCGGGACGAGAAACGGACTGA																				
												106								
G	N	L	P	/ ^G	С	S	F	S	Ι	F	L	L	A	Ь	ь	S	C	بل	Τ΄	186
CTC	יכככ	GCT	$\neg c k$	GCC	ጥልር	יר א א	CTC	רכר	יא ארי	92	0									
CAC		CGA	AYT	.CGG																
V	P	A	Þ	A	Y	Q	V	R	N	19	6									

SEQ ID No 2. - HCV Core Protein - Amino acids 125 to 144

ACCCTTACGTGCGGCTTCGTCGATCTCATGGGGTACATACCGCTCGTCGGCGCCCCTCTT 777
TGGGAATGCACGCCGAAGCAGCTAGAGTACCCCATGTATGGCGAGCAGCCGCGGGGAGAA
T L T C G F V D L M G Y I P L V G A P L 144

SEQ ID No 3. - HCV Core Protein - Amino acids 161 to 166

GGTGTGAACTATGCAACA 840 CCACACTTGATACGTTGT G V N Y A T 166

SEQ ID No.4 - human ADRP - nucleotide sequence

 $\tt CGTCTTCGGGACGCCCGCTCTTCGCCTTTCGCTGCAGTCCGTCGATTTCTTCTCCAGGCGCCGCTCTTCGCCTGCAGTCCGTCGATTTCTTCTCCAGGCGCTCGATTTCTTCTCCAGGCCTCTTCGCTGCAGTCCGTCGATTTCTTCTCCAGGCCTCTTCGCTGCAGTCCGATTTCTTCTCCAGGCTCGAGTCCGATTTCTTCTCCAGGCCTCGAGTCCGAGTCCGATTTCTTCTCCAGGCCTCGAGTCCAGGCCGCTCTTCGCTGCAGGCCGAGTCCGATTTCTTCTCCAGGCCTCGAGTCCGAGTCCGAGTCCAGGCAGGCAGGCCAGGCAG$ 60 GAAGAAAAATGGCATCCGTTGCAGTTGATCCACAACCGAGTGTGGTGACTCGGGTGGTCA ACCTGCCCTTGGTGAGCTCCACGTATGACCTCATGTCCTCAGCCTATCTCAGTACAAAGG 180 ACCAGTATCCCTACCTGAAGTCTGTGTGTGAGATGSCAGAGAACGGTGTGAAGACCATCA CCTCCGTGGCCATGACCAGTGCTCTGCCCATCATCCAGAAGCTAGAGCCGCAAATTGCAG 300 TTGCCGATACCTATGCCTGTAAGGGGCTAGACAGGATTGAGGAGAGACTGCCTATTCTGA 360 ATCAGCCATCAACTCAGATTGTTGCCAATGCCAAAGGCGCTGTGACTGGGGCAAAAGATG 420 CTGTGACGACTACTGTGACTGGGGCCAAGGATTCTGTNGCCAGCACGATCACAGGGGTGA 480 TGGACAAGACCAAAGGGGCAGTGACTGGCAGTGTGGAGAAGACCAAGTCTGTGGTCAGTG 540 GCAGCATTAACACAGTCTTGGGGAGTCGGATGATGCAGCTCGTGAGCAGTGGCGTAGAAA 600 660 TAGAAAAAGAAGCAAAAAAAGTTGAAGGATTTGATCTGGTTCAGAAGCCAAGTTATTATG 720 TTAGACTGGGATCCCTGTCTACCAAGCTTCACTCCCGTGCCTACCAGCAGGCTCTCAGCA 780 840 GGGTTAAAGAAGCTAAGCAAAAAAGCCAACAGACCATTTCTCAGCTCCATTCTACTGTTC 900 ACCTGATTGAATTTGCCAGGAAGAATGTGTATAGTGCCAATCAGAAAATTCAGGATGCTC 960 AGGATAAGCTCTACCTCTCATGGGTAGAGTGGAAAAGGAGCATTGGATATGATGATACTG 1020 ATGAGTCCCACTGTGCTGAGCACATTGAGTCACGTACTCTTGCAATTGCCCGCAACCTGA 1080 CTCAGCAGCTCCAGACCACGTGCCACACCCTCCTGTCCAACATCCAAGGTGTACCACAGA 1140 ACATCCAAGATCAAGCCAAGCACATGGGGGGTGATGGCAGGCGACATCTACTCAGTGTTCC GCAATGCTGCCTCCTTTAAAGAAGTGTCTGACAGCCTCCTCACTTCTAGCAAGGGGCAGC 1200 TGCAGAAAATGAAGGAATCTTTAGATGACGTGATGGATTATCTTGTTAACAACACGCCCC 1260 1320 -58- P5523GB

AAGGTGCAGAGATGGACAAGAGCAGCCAGGAGACCCAGCGATCTGAGCATAAAACTCATT 1380 1440 1500 GAAATTAACTTGCTAGGCAACCCTAAATTGGGAAGCAAGTAGCTAGTATAAAGGCCCTCA 1560 ATTGTAGTTGTTTCCAGCTGAATTAAGAGCTTTAAAGTTTCTGGCATTAGCAGATGATTT CTGTTCACCTGGTAAGAAAAGAATGATAGGCTTGTCAGAGCCTATAGCCAGAACTCAGAA 1620 AAAATTCAAATGCACTTATGTTCTCATTCTATGGCCATTGTGTTGCCTCTGTTACTGTTT 1680 GTATTGAATAAAAACATCTTCATGTGGGCTGGGGTAGAAACTGGTGTCTGCTCTGGTGTG 1740 1800 GTTTTTCATTTCTCAAATAGGAATACTACCTTTGAATTCAATAAAATTCACTGCAGGATA 1860 GACCAGTTNAGNAGCAAACANNCANGTACACNNAAGANAC 1900

SEO ID No. 5 - human ADRP - Amino acid sequence

MetAlaSerValAlaValAspProGlnProSerValValThrArgVal 16 32 ValAsnLeuProLeuValSerSerThrTyrAspLeuMetSerSerAla TyrLeuSerThrLysAspGlnTyrProTyrLeuLysSerValCysGlu 48 MetXaaGluAsnGlyValLysThrIleThrSerValAlaMetThrSer 64 AlaLeuProIleIleGlnLysLeuGluProGlnIleAlaValAlaAsp 80 ThrTyrAlaCysLysGlyLeuAspArgIleGluGluArgLeuProIle 96 LeuAsnGlnProSerThrGlnIleValAlaAsnAlaLysGlyAlaVal 112 ThrGlyAlaLysAspAlaValThrThrThrValThrGlyAlaLysAsp 128 SerValAlaSerThrIleThrGlyValMetAspLysThrLysGlyAla 144 ValThrGlySerValGluLysThrLysSerValValSerGlySerIle 160 AsnThrValLeuGlySerArgMetMetGlnLeuValSerSerGlyVal 176 GluAsnAlaLeuThrLysSerGluLeuLeuValGluGlnTyrLeuPro 192 LeuThrGluGluGluLeuGluLysGluAlaLysLysValGluGlyPhe 208 224 AspLeuValGlnLysProSerTyrTyrValArgLeuGlySerLeuSer ThrLysLeuHisSerArgAlaTyrGlnGlnAlaLeuSerArgValLys 240 ${\tt GluAlaLysGlnLysSerGlnGlnThrIleSerGlnLeuHisSerThr}$ 256 ${\tt ValHisLeuIleGluPheAlaArgLysAsnValTyrSerAlaAsnGln}$ 272 LysIleGlnAspAlaGlnAspLysLeuTyrLeuSerTrpValGluTrp 288 LysArgSerIleGlyTyrAspAspThrAspGluSerHisCysAlaGlu 304 HisIleGluSerArgThrLeuAlaIleAlaArgAsnLeuThrGlnGln 320

-59-	P5523GE
LeuGlnThrThrCysHisThrLeuLeuSerAsnIleGlnGlyValPro	336
GlnAsnIleGlnAspGlnAlaLysHisMetGlyValMetAlaGlyAsp	352
IleTyrSerValPheArgAsnAlaAlaSerPheLysGluValSerAsp	368
SerLeuLeuThrSerSerLysGlyGlnLeuGlnLysMetLysGluSer	384
LeuAspAspValMetAspTyrLeuValAsnAsnThrProLeuAsnTrp	400
LeuValGlyProPheTyrProGlnLeuThrGluSerGlnAsnAlaGln	416
AspGlnGlyAlaGluMetAspLysSerSerGlnGluThrGlnArgSer	432
CluHisLysThrHis	437